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## ALIGNMENTS

KFHU7 RESULT 1

A;Cross-references: GDB:119897; OMIM:227500 A;Map position: 13q34-13q34 A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1 R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pe J. Biol. Chem. 266, 11051-11057, 1991
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylation A;Reference number: A40529; MUID:91250411; PMID:1904059
A;Contents: annotation; carbohydrate binding sites Eur. J. Blochem. 234, 293-300, 1995
A;Title: Structurally and functionally distinct Ca(2+) binding sites
A;Reference number: S63524; MUID:96096752; PMID:8529655
A;Recession: S63524 A; Molecule type: protein A; Residues: 213-466 <TH2> A;Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801 R;Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, Blochemistry 27, 7785-7793, 1988 A;Title: Amino acid sequence and posttranslational modifications of human factor VII-A;Reference number: A90539; MUID:89088153; PMID:3264725 A;Accession: A31186 A:Cross-references: GB.J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334 R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986 A:Title: Characterization of a cDNA coding for human factor VII. A:Reference number: A23819; MUID:86205965; PMID:3486420 A:Accession: A23819 cobgulation factor VIIa (EC 3.4.21,21) precursor [validated] - human c;Species: Homo sapines (man) C;Date: 19-May-1989 #sequence\_revision 19-May-1994 #text\_change 08-Dec-2000 C;Accession: A28322; A23819; A31106; B31186; S63524 R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987 A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep A;Reference number: A28322; MUID:87260948; PMID:3037537 A;Accession: A28322 A; Gene: GDB:F7 C; Genetics: A; Molecule type: protein A; Residues: 61-65;99-103;105-109;213-217;308-312 <PER> R; Persson, E.; Petersen, L.C. A; Molecule type: protein A; Residues: 61-212 <THI> A; Accession: B31186 A; Molecule type: mRNA A; Residues: 1-466 <HAG> A; Molecule type: DNA A; Residues: 1-466 <0 1-466 <OHA> in the gamma-car Hart

A; Description: catalyzes the proteolytic activation of coagulation oagulation factor IX in the presence of calcium and tissue factor

factor X in the pr

C; Function:

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A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Reywords: beta-hydroxyaspartic acid: blood coagulation; calcium binding; carboxyglutam
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-60/Domain: propeptide #status predicted <PRO>
F;45-104/Domain: Gla domain homology <GLA>
F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;11-214/Domain: EGF homology <EG1>
F;110-141/Domain: EGF homology <EG2>
F;213-465/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;213-447/Domain: EGF homology <EG2>
F;213-447/Domain: trypsin homology <EG2>
F;213-447/Domain: trypsin homology <EG2>
F;110-121/Li5-130,132-141,151-162,158-172,174-187,195-22,219-224,238-254,370-389,
F;112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;205,382/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;205,382/Binding site: Arg-Ile (coagulation factor XIIa) #status experimental
F;212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;253,302,444/Accive site: Arg-Gly (coagulation factor Xa) #status predicted
Coagulation factor VII - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
C;Accession: 146932
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A;Title: Complete nucleotide sequence of the cDNA encoding rabb,
A;Reference number: 146932; MUID:93190306; PMID:8383365
A;Accession: 146932
A;Accession: 146932
A;Molecule type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:9266294; PID:9266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:9266294; PID:9266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
A;Cross-references: GB:S56300; NID:9266294; PID:9266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
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C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
A;Residues: 1-443 <BRO>
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C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:9266294; PID:9266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain her; As a complete type: mRNA
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Pred. No. 4.4e-154;
0; Mismatches 10;
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Pred. No. 6.4e-1
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A;Description: catalyzes the proteolytic activation of coagulation factor X in the prigulation factor IX in the presence of calcium and tissue factor A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; cypords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
F;1-152/Product: coagulation factor VIIa light chain *status experimental <MA1>
F;1-44/Domain: Gla domain homology (fragment) <GLA>
F;50-81/Domain: EGF homology <EG2>
F;51-127/Domain: EGF homology <EG2>
F;153-407/Product: coagulation factor VIIa heavy chain *status experimental <MA2>
F;153-387/Domain: trypsin homology <FRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Moleonia *****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Residues: 58-62, 'X', 64-68 <MCM>
A; Residues: 58-62, 'X', 64-68 <MCM>
A; Rote: the residue designated 'X' was determined to be hydroxyaspar
R; Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; M
B; Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; M
J, Blochem. 104, 867-868, 1988
A;Tille: A new trisaccharide sugar chain linked to a serine residue
A; Reference number: A44556; MUID:89213999; PMID:3149637
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: structure and location of covalently bound C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Takeya, H.; Kawabata, S.; Nakagawa, J. Biol. Chem. 263, 14868-14877, 1988 A;Title: Bovine factor VII. Its purif; A;Reference number: A31979; MUID:89008 A;Accession: A31979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor VIIa (EC 3.4.21.21) - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 C;Accession: A31979; C20274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-407 < TAK> R; McMullen, B.A.; Fujika
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Sueyoshi, T.; Miyata,
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A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the protection coagulation
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan
                                                                                                                                                                         A; Molecule type: protein A; Residues: 41-55 <GO2> A; Accession: S20381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999 C;Accession: S15838; S20380; S20381 R;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogas FEBS Lett. 283, 281-285, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation factor Xa (EC 3.4.21.6) precursor - chicken N; Alternate names: virus-activating proteinase C; Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                        A; Title: Isolation of factor Xa from chick embryo as the amniotic A; Reference number: $20380; MUID:92164779; PMID:1537403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Primary structure of the virus activating protease A; Reference number: S15838; MUID:91257322; PMID:2044767
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                                                                                                                          A; Molecule type: protein A; Residues: 241-246, 'X', 248-251, 'X', 253-261
                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
R;Gotoh, B.; Yamauch1, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-475 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: not compared with conceptual translation
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Pred. No. 2.4e-109;
5; Mismatches 75;
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C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
C;Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
C;Accession: A24478; JQ0917; A42485; A25853; A22208; A21284; A20362; S39415;
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
Biochemistry 25, 5098-5102, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organ
A;Reference number: A24478; MUID:87026600; pMID:3768336
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F;21-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-185/Product: coagulation factor x light chain #status experimental <LCH>
F;41-185/Product: coagulation factor x light chain #status predicted <HCH>
F;90-121/Domain: EGF homology <EGI>
F;186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-475/Product: coagulation factor X heavy chain #status experimental <AHC>
F;186-240/Domain: activation peptide #status predicted <APT>
F;241-475/Product: coagulation factor X heavy chain #status experimental <AHC>
F;241-475/Product: coagulation factor X heavy chain #status experimental <AHC>
F;241-475/Product: coagulation factor X heavy chain #status experimental <AHC>
F;241-465/Domain: trypsin homology <TRY
F;241-465/Domain: trypsin homology <TRY
F;241-465/Domain: trypsin homology <TRY
F;464-7,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)
F;762,90-101,95-110,112-121,129-140,136-152,154-167,175-38,247-252,267-283,396-410
F;103/Modified site: exthro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,328,425/Active site: H1s, Asp, Ser #status predicted
A;Cross-references: GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; R;MesSier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R. Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA enva;Reference number: JQ0917; MUID:91216473; PMID:1902434
A;Accession: JQ0917
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-488 <LEY>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATVGHFGVYTRVSQYIEWLQKLMRSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILTAAHCINOSK---EIKVVVGEVDREKEEHSETTHTAEKIFVHSKYIAETYDNDIALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKDOLOSYICFCLPAFEGRNCETHKDDQLI----CVNENGGCEQYCSDHTGTKRS---CRCH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLKEPIQFSEYVVPACLPQADFANEVLMNQKSGMVSGFGREFEAGRLSKRLKVLEVPYVD
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                                                                        encoding human
                                                                                                                                                                                        PID: g182831
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A:Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330 R; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; J. MOl. Biol. 232, 947-966, 1993 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resoluti A; Reference number: A49458; MUID:93360277; PMID:8355279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. E
A; Title:
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A;Note: Sequence extracted from NCBI Dackbook
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.;
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of
A;Title: Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushana Gene 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon A; Reference number: 154051; MUID:90128299; PMID:2612918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 183-234 < INO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: mRNA
A:Residues: 19-284 (E', 289-488 <RAU>
A:Residues: 19-284 (E', 289-488 <RAU>
A:Residues: 19-284 (E', 289-488 <RED: RID: 180335; PIDN:AAA51984.1;
A:Coss-references: GB:M22613; NID:g180335; PIDN:AAA51984.1;
R:Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A:Title: Characterization of an almost full-length cDNA codir
A:Reference number: A22208; MUID:85216545; PMID:2582420
A:Accession: A22208
                                                                  A; Map position:
                                                                                        A; Cross-references: GDB:119890; OMIM:227600
                                                                                                                               A; Gene: GDB:F10
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-23 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: identification and characterization of beta-hydroxyaspartic R; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lym
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A;Residues: 13-441,'S', 443-488 <FUN>
A;Cross-references: GB:KO3194; NID:g182840; PIDN:AAA52490.1;
R:Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:McMullen, B.A.; Fujikawa, K.; Kisiel, Biochemistry 22, 2875-2884, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 13-284,'E',289-488 <LE2>
A;Cross:references: GB:K01886
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A:Title: Liver-specific expression of the gene coding for hund; Reference number: A42485; MUID:92218390; PMID:1313796
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A; Residues: 1-488 <MES>
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A; Residues: 1-15 <MIA>
                                                                                                                                                                                Comment: The two chains
                                                                                                                                                           Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JE, K.; Morita, T.

J. Biochem. 218, 153-163, 1993

J. Biochem. 218, 153-163, 1993

Le: Identification of O-linked oligosaccharide chains

le: number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete amino
                                                                                                                                                           The two chains held together by one disulfide bond are formed from a single-distribution. Service is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mino acid sequence of the light chain of human A20362; MUID:83257207; PMID:6871167
                        86/1; 124/1; 150/3; 249/3; 289/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from NCBI backbone (NCBIN:93780,
B.; Roberts, S.; Jagadeeswaran, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.; Sasagawa, T.; Howald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMID:6587384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for human
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E.W.
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Congulation factor IXa (EC 3.4.21.22) precursor - bovine
N;Alternate names: Christmas factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 03-Aug-1984 #text_change 16-Jul-1999
C;Accession: A14757; B20274; I45891; A00923
R;Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A;Title: Comparison of amino acid sequence of bovine coagulation factor IX (Chriat; Reference number: A14757; MUID:80056619; PMID:291916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:183-234/Domain: activation peptide #status experimental <APT>
F:235-488/Product: coagulation factor Xa heavy chain #status experimenta
F:235-462/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;41-179/Product: coagulation factor X light chain #status experimental <LCH> F;90-121/Domain: EGF homology <EG1> F;129-164/Domain: EGF homology <EG2> F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;57-62/Disulfide bonds: #status predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;24-40/Domain: propeptide #status predicted <PRO>F;25-84/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: coagulation factor x; EC
C; Keywords: beta-hydroxyaspartic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: deficiency of this factor causes Stuart disease C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: catalyzes the proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199,211/Binding site: carbohydrate (Thi) (covalent) #status experimental 221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental 234-235/Cleavage site: Arg-lie (coagulation factor IXa, coagulation factor VIIa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103/Modified site: erythro-beta-hydroxyaspartic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homo; Keywords: beta hydroxyaspartic acid; blood coagulation; calcium binding; carboxyg
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         447
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GKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKDQLQSYICFCLPAFEGRNCE--THKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGY 118
                                           GHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAP 404
                                                                                                                          QQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATV
                                                                                                                                                                     ITFRMNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSC-
                                                                                                                                                                                                                VVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCL
                                                                                                                                                                                                                                                                                                                                                   FDLLDFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTA
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                                                                                                                                                                                                                                                           AHCLYQAKRFK---VRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTP
                                                                                                                                                                                                                                                                                                      AHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLLADGVSCTPTVEYPCGKIPILEKRNASKPQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKDGLGEYTCTCLEGFEGKNCELFTRK----LCSLDNGDCDQFCHEEQNSV-VCSCARGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDQCETSFCQNQGK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                 -KLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARK 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 858.5; DB : Pred. No. 1.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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    479
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(Christmas

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A;Description: catalyzes the proteolytic activation of coagulation factor X in the prese A;Pethway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium 5inding; carboxyglutam
F;1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
F;1-45/Domain: Gla domain homology (fragment) <GLa>
F;1-81/Domain: EGF homology <EG2>
F;147-181/Domain: EGF homology <EG2>
F;187-181/Domain: EGF homology <EG2>
F;182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;182-409/Domain: trypsin homology <TRY>
F;182-409/Domain: trypsin homology <TRY>
F;182-3,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-551,362-390/Disulfide
F;53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;222,270,366/Active site: His, Asp, Ser #status predicted
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 52-139 <CCHO>
A;Cross-references: GB.J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1998
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa;
A;Reference number: A44556; MUID:89213999; PMID:3149637
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Blochen. Biophys. Res. Commun. 115, 8-14, 1983
B;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood A;Reference number: A20274; MUID:B3308813; PMID:6688526
A;Accession: B20274
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A;Molecule type: protein
A;Residues: 1-63,'T',65-
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A;Residues: 59-63,'X',65-69 <MCM>
R;Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 299, 178-180, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: structure and location of a carbohydrate covalently bound to Ser C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strockscore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                              277
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                                                                                                                                                                                                                                               VEYPCGKIPI - - LEKR - - .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNIERECKEEKCSFEEAREVFENTEKTTEFWKQYYDGDQCESNPCLNGGMCKDDINSYEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYIC
                               RF--SLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSD 334
                                                                                             TEQKRNVIRAIPYHSYNASINKYSHDIALLELDEPLELNSYVTPICIADRDY---TNIFS
                                                                                                                                                        DEQSRRVAQVIIPSTYVPGTT--NHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV 276
                                                                                                                                                                                                                                                                                                                                   VPFPCGRVSVSHISKKLTRAETIFSNTNYENSSEAEIIWDNVTQSNQSFDEFSRVVGGED 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WCQAGFEGTNCEL----DATCSIKNGRCKQFCKRDTDNKVVCSCTDGYRLAEDQKSCEPA
                                                                                                                                                                                                                AERGQFPWQVLLHGEIAAFCGGSIVNEKWVVTAAHC---IKPGVKITVVAGEHNTEKPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.9%; Score 850.5; DB 1; Length 416; Larity 40.2%; Pred. No. 5:1e-56; Conservative 68; Mismatches 129; Indels 51
         ,65-416 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                               ---NASKPQ------GRIVGGKV 158
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                                                 A; Molecule type: mRNA
A; Residues: 38-193, 'T', 195-326
A; Cross-references: GB:M35672
R; Kurachi, K.; Davie, E.W. Proc. Natl. Acad. Sci. U.S
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A; Residues: 1-461 < ANS>
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A; Residues: 1-461 < YOS>
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A;Cross references: GB:KO2048
R;Reltsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
A;Rifle: The putative factor IX gene promoter in hemophilia B Leyden.
A;Rifle: The putative factor IX gene promoter in hemophilia B Leyden.
A;Rifle: The putative factor IX gene promoter in hemophilia B Leyden.
A;Rifle: The putative factor IX gene promoter in hemophilia B Leyden.
A;Residues: 8-24 cREI>
A;Recession: A30511; MUID:88327116; PMID:3416069
A;Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
A;Cross-references: EMBL:X55008; NID:g4469253
A;Cross-references: EMBL:X55008; NID:g44692
                                                                                        A; Molecule type: mRNA
A; Residues: 1-193, 'T, 195-461 <JAY>
A; Kesidues: 1-193, 'T, 195-461 <JAY>
A; Cross-references: GB.J00137; NID:9182610; PIDN:AAA52763.1;
A; Cross-references: GB.J00137; NID:9182610; PIDN:AAA52763.1;
Comat. Cell Mol. Genet. 10, 465-473, 1984
A; Title: Isolation and characterization of human factor IX clay Reference number: A37546; MUID:84300526; PMID:6089357
A; Accession: A37546
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A; Reference number: A22673; MUID:85190593; pMID:3857619
A; Rolecule type: mRNA
A; Residues: 1-193, 'T', 195-461 <MCG>
A; Residues: 1-193, 'T', 195-461 <MCG>
A; Ross references: GB:M11309; NID:9180552; PIDN:AAA52023.1; PID:9180553
A; Note: the authors translated the codon ACA for residue 29 as Tyr
R; Jaye, M; de la Salle, H; Schamber, F; Balland, A; Kohli, V; Findeli, A.; Tolst Nucleic Acids Res. 11, 2325-2335, 1983
A; Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52
A; Reference number: A21337; MUID:83220788; PMID:6687940
A; Accession: A21337
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C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence_revision 30-Jun-1987 #text_change 15-Sep-2000
C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486;
R;Yoshitake, S; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3735-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor A;Accession: A00922; MUID:86000558; PMID:2994716
A;Accession: A00922
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A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:84236100; PMID:6329734
A;Accession: A37570
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Warren, S.T.
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A;Accession: 159512
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 444-461 CRES>
A;Cross:references: GB:S66752; NID:g439773;
A;Cross:references: Koeberl, D.D.; Sarkar, G.;
                                     A:Molecule type: protein
A:Molecule type: protein
A:Residues: 'D', 204,'X', 206-211;212,'D', 214,'X',216-221,'D'
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A; Residues: 290-359 <RE2>
A; Cross references: GB: M19063; NID: g182622;
A; Cross references: GB: M2063; NID: g182622;
                                                                                                                    A:Title: Activation peptide
A:Reference number: A54255;
A:Accession: A54255
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A; Residues: 92-130 <HAN>
A; Residues: 92-130 <HAN>
A; Note: NMR detection of calcium binding by domain expressed
R; de la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A
Thromb. Haemost. 70, 370-371, 1993
A; Title: A deletion located in the 3' non translated part of
A; Reference number: IS9612; MUID:94054330; PMID:8236150
                                                                                                                                                                                                                                                                                                                   A;Reference number: I59529;
A;Accession: I59529
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A;Title: The first EGF-like domain from human factor IX

A;Title: The first EGF-1 MUID: 90151623; PMID: 2406129
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A; Residues: 105-109, 'x', 111-115
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Blochem. Blophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: A20274
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A;Title: Development of an immunoaffinity process for fA;Reference number: A60486; MUID:90194857; PMID:2316207
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A;Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
A;Experimental source: liver
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kawa, K.; Kisiel, V
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8; MUID:91006024; PMII
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MUID:94227047; F
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PMID:2209546
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Shimonishi, Y.; N
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F;47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F;97-128/Domain: EGF homology <EG1>
F;192-126/Domain: EGF homology <EG2>
F;192-226/Domain: activation peptide #status experimental <ACT>
F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
F;227-461/Domain: trypsin homology <TRY>
F;327-454/Domain: trypsin homology <TRY>
F;33,54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu F;64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-335,252-268,382-396,407-4:
F;99/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                  F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental F;203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental F;205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental
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A;Title: Blood clotting factor IX B(M) Nagoya: substitution A;Title: Blood clotting factor IX B(M) Nagoya: substitution A;Reference number: A30622; MUID:9007829; PMID:2592373
A;Contents: annotation; sequence of mutant B(M) Nagoya A;Note: carboxylation; sequence of mutant B(M) Nagoya A;Note: carboxylation; glycosylation, and cleavage sites R;Baron, M; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayh submitted to the Brookhaven protein Data Bank, November 1991 A;Reference number: A51252; PDB:1IXA A;Contents: annotation; conformation by (1)H-NMR, residues 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Pathway: blood coagulation intrinsic pathway C;Superfamily: coagulation factor X; EGF homology; Gla domain C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calc F;1-28/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: recombinant form expressed in yeast C;Comment: Factor IX is activated by factor XIa, which excises the activation C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gia) residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F; 29-46/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:119900; OMIM:306900
A;Map position: Xq27.1-Xq27.2
A;Introns: 30/1; 84/2; 93/1; 131/1; 174/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: annotation; signal sequence cleavage site R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J. Biol. Chem. 264, 21257-21265, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;39-46/Domain: propeptide #status experimental <PPT>F;31-91/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Pescription: catalyzes the proteolytic activation of coagulation factor x in the A; Pathway: blood coagulation intrinsic pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Jo
J. Biol. Chem. 259, 5698-5704, 1984
A;Title: Derivatives of blood coagulation f
A;Reference number: A37543; MUID:84185715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB:F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Morita, T.; ]
J. Biol. Chem.
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A;Reference number: A18483; MUID:78194509; PMID:659613
A;Contents: annotation; activation; active site; carbohydrate
R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A37544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: 194-Thr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
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Best Local
                                                                                                                                            226-227/Cleavage site:
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                       161;
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Chem. 260, 2583, 1985
                                                  Similarity
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r: A37569
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                                                                                                                                     Arg-Val (coagulation
                                        38.8%;
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                                           Score 849;
Pred. No. 7
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          Mismatches
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                                    DB 1;
7.4e-56;
                                                                                                                              factor XIa) #status
                                                               Length
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1991
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Gaps
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A:Molecule type: protein
A:Molecule type: protein
A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492
A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492
A:Rote: carbohydrate binding sites and disulfide bonds were determined
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A;Biol. Chem. 264, 16897-16904, 1989
A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 41-102,'N',104-180 <ENF>
R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Baphys. Res. Commun. 115, 8-14, 1983
A; Title: The occurrence of beta-hydroxyaspartic acid in the vitami A; Reference number: A20274; MUID:8308813; PMID:6888526
A; Contents: annotation; revision to residue 103
R; Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A; Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of A; Reference number: A12030; MUID:76053069; PMID:1059093
A; Accession: A12030
                                              Eur. J. Blochem. 218, 153-163, 1993
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides
A:Reference number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                            A; Molecule type: protein
A; Residues: 85-126 <PER>
A; Note: beta-hydroxyaspartic acid site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor x mRNA encodes a single polypeptide chain containing A;Reference number: A22867; MUID:84247315; PMID:6330671
A;Accession: A22867
                                                                                                                                       R; Inoue, K.; Morita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor). A;Reference number: A14997; MUID:80130563; PMID:6766735
A;Accession: A14997
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type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLDK 389
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              145 NASKPQG----
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165; Conserv
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F;41-160/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;129-164/Domain: EGF homology <EG2>
F;183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-233/Domain: activation peptide #status experimental <AHC>
F;183-233/Domain: activation factor Xa heavy Chain #status experimental <AHC>
F;234-492/Product: coagulation factor Xa heavy Chain #status experimental <AHC>
F;234-492/Product: coagulation factor Xa heavy Chain #status experimental <AHC>
F;234-461/Domain: trypsin homology <TRY>
F;246-47,260-276,389-403,414-442/Disulfide bonds: #status experimental
F;215,321,418/Active site: His, Asp, Ser #status predicted
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A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carbo
A;Reference number: A38024; MUID:84185716; PMID:6546930

A;Contents: annotation; calcium binding

T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: The two chains are formed from a single-chain precursor by the exc
C;Comment: The two chains are formed from a single-chain precursor by the exc
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Contents: annotation; active site
R;Fujikawa, K; Titani, K; Davie, E.W.
Proc. Natl Acad. Sci. U.S.A. 72; 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor):
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
J. Biol. Chem. 259, 5705-5710, 1984
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Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-1a (activated Stuart factor). E
A;Reference number: A12453; MUID:73053314; PNID:4264286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: Calcium binds to the gamma-carboxyglutamic acid c;Comment: The gamma-carboxyglutamic acid residues arise by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 183-196;199-209;216-233 <INO>
A;Note: carbohydrate binding sites
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                                                                                                                                                       GDDSKSCVSTERFPCGKFTQGRSRRWAIHTSEDALDASELEHYDPADLSPTESSLDLLGL
                                                                                                                                                                                                                                                                                                                                                                    CKDGIGDYTCTCAEGFEGKNCEFSTRE--ICSLDNGGCDQFCREERSEVR-CSCAHGYYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.5%; Score 843; DB 1; 37.7%; Pred. No. 2.2e-55;
RIVGGKVCPKGECPWQVLLL-VNGAQLCGGTLINTIWVVSAAHCF
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a posttranslational, vita
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A; Modacule type: DNA
A; Residues: 295-383, 'G', 385-455 <MUR>
A; Cross-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
C; Function:
A; Description: Catalyzes the proteolytic activation of prothrombin to thrombin in the proteolytic activation of prothrombin to thrombin in the proteolytic activation of prothrombin to thrombin in the proteolytic activation factor X; EGF homology; Gla domain homology; trypsin homology; C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam; F; 1-37 Domain: signal sequence #status predicted <SIG>F; 24-40 Domain: Signal sequence #status predicted <SIG>F; 25-84 Domain: Gla domain homology <GLA>F; 41-179 Product: coagulation factor X light chain #status predicted <LCH>F; 90-121/Domain: EGF homology <EGI>F; 90-121/Domain: EGF homology <EGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type; protein
A; Mesidues: 183-186, 7188-207 <ENJ2>
A; Residues: 183-186, T.; Kamura, T.; Kuroiwa, M.; Harada, M.;
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.;
Eur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences and deduced A; Reference number: 146196; MUID:94222160; PMID:8168596
A; Accession: 162745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Characterization of rat factors X and Xa: demonstration A;Reference number: PS0190; MUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601 A:Note: submitted to the EMBL Data Library, June 1994 A:Note: neither the complete nucleic acid sequence nor the complete transl gene 109; Ross, R.P.; Hutson, S.; Wallin, R. gene 109; 209-273, 1996 A:Title: Processing and expression of rat and human clotting factor-X-enco A:Reference number: JC4670; MUID:96194815; PMID:8647460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors A;Reference number: A58498; MUID:96093366; PMID:8578539
A;Accession: S49075
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A:Residues: 1-482 <STA2>
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A; Residues: 1-482 <STAl>
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Residues: 41-58,'X',60-65 <ENJ1>
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;Species: Rattus norvegicus (Norway rat)
;Datte: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000;Accession: S49075; JC4670; PS0191; PS0190; I62745
;Rocession: Ross, P.; Hutson, S.; Wallin, R.
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RESULT
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F;46,47,54,56,59,60.65,66,9,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-40
F;103/Modified site: carbohydrate (Asn) (covalent) #status predicted
F;107/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;208/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218/Binding site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #
F;274,320,417/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                     257 HVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRK
                                                                                                                                                                                                                                                                                                        278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                YTKVTAFLKWIDRSMKARVGP 470
                                                                                                                                                                                                               NVAPAČLPQKDWAEATLMTQKTGIVSGFGRTHEKGRQSKVLKMMEVPYVDRNTC----R
                                                                                                                                                                                                                                                                                         QAKREK----VRVGDLNTEQEDGGEMVHEVDMIIKHNKFQRDTYDFDIAMLRLKTPITFRE
                                                                                                                                                                                                                                                                                                                              KIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                               GNDGKSCLSTAPFPCGKTNKGRAKRSVALNTSNSEPDPEDLMPDADILYPTESPSELLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRDGLGSYTCTCTEGFEGKNCELFV--RKLCSLDNGDCDQFCREEQNSV-VCSCAKGYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTTEFWNKYEDGDQCESSPCQNQGE
                                                                                                        YTRVSQYIEWLQKLMRSEPRP
                                                                                                                                      LSTSFSITQNMFCAGYDAKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGI
                                                                                                                                                                                                                                                                                                                                                                    NKTEPEANSDDVIRIVGGQECKRGECPWQALLFSDEETDGFCGGTILNEFYILTAAHCLH
                                                                                                                                                                                                                                                                                                                                                                                          NASKPOG------RIVGGKVCPKGECPWQVLLLVNGAQ--LCGGTLINTIWVVSAAHCFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADGVSCTPTVEYPCGKI-----
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36.1%;
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Pred. No. 1.6e-54;
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R;Wu, S.M.; Stafford, D.W.; Gene 86, 275-278, 1990 A;Title: Deduced amino acid A;Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629 A;Experimental source: liver R;SarKar, G.; Koeberl, D.D.; Sommer, S.S. Genomics 6, 133-143, 1990 A;Title: Direct sequencing of the activation peptide and A;Reference number: 146580; MUID:90152675; PMID:2303254 A;Accession: 149667 C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence\_revision
C:Accession: JQ0419; 149667
R:Wu, S.M.; Stafford, D.W.; Ware, J. A; Status: preliminary; translated A; Molecule type: mRNA A; Residues: 1-459 < WUS> A; Reference number: JQ0419; A; Accession: JQ0419 coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment) mRNA sequence of mouse blood-coagulation MUID:90215309; PMID:2323576 from GB/EMBL/DDBJ 07-Sep-1990 PIDN: AAA37629.1; #text\_change 16-Jul-1999 the catalytic domain of PID: 9387158 factor

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coagulation factor IXa (EC 3.4.21.22) precursor - C:Species: Canis lupus familiaris (dog) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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R;EVANDS, J.P.; Watzke, H.H.; Ware, J.L.; Stafford, D.W. Blood 74, 207-212, 1989
A;Title: Molecular cloning of a cDNA encoding canine face A;Reference number: A30351; MUID:89323338; PMID:2752110
A;Accession: A30351
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F;85-116/Domain: EGF homology <EG1>
F;12-158/Domain: EGF homology <EG2>
F;122-158/Domain: EGF homology <EG2>
F;225-452/Domain: EGF homology <EG2>
F;225-452/Domain: EGF homology <EG2>
F;225-452/Domain: trypsin homology <TRY>
F;41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) *s
F;52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/Dis
F;265,313,409/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 168-362,'Q',364-387,'I',389-451 <RES>
A;Cross references: GB:M26236; NID:g193319; PIDN:AAA37630:1; PID:g193320 C;Comment: This protein plays a critical role in blood coagulation. C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; try C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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F:19-79/Domain: Gla domain homology <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 GSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSQYIEWLQK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NITEY--MFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERTFSERTLAFVRF:-SLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTN---HDIALLRLHQPVVLTEHVVPLCL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPFPCGRASISYSSKKITRAETVFSNMDYENSTEAVFIQDDITDGAILNNVTESSESLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFTTYNNMFCAGYREGGKDSCEGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANR----EYTNIFLKFGSGYVSGWGKVFNKGRHASILQYLRVPLVDRATCLR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WCQVGFEGRNCEL ----DATCNIKNGRCKQFCKNSPDNKVICSCTEGYQLAEDQKSCEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSRYVNWIKE 454
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Pred. No. 5.4e-54;
7; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                       D.W.; High,
                                                                                                                                                                                                                                              factor
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                                                skin
                                                                                                           PID:g163948
                                                fibroblasts
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Matches

Similarity

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Conservative

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Indels

Gaps

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274

Score 781; DB 2; Pred. No. 3e-51; 3; Mismatches 10

EHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLA

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A; Molecule type: DNA A; Residues: 1-159 < RES>
A; Residues: 1-159 < RES>
A; Cross-references: GB:D21212; NID:g415306; PIDN:BAA04753.1; PID:g455394
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; F;1-159/Domain: trypsin homology (fragment) < TRY>
                                                                                                                        A;Reference number: 146196; MUID:94222160; p
A;Accession: 184615
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F:90-121/Domain: EGF homology <EG1>
F:127-163/Domain: EGF homology <EG2>
F:127-163/Domain: EGF homology <FG2>
F:218-445/Domain: EGF homology <TRY>
F:218-445/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)
F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M33826; NID:g163949; PIDN:AAA30844.1; PID:g163950
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; tr;
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding;
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                              Eur. J. Haematol. 52, 162
A; Title: Analysis of the
                                                                                                                                                                                                                    R; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa,
                                                                                                                                                                                                                                                                                                                coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-452 < AXE>
                                                                                                                                                                                                                                           oagulation factor VII - rhesus macaque (fragment);Species: Macaca mulatta (rhesus macaque);Date: 02-Aug-1996 #sequence_revision 02-Aug-1996;Accession: I84615
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Best Local Similarity .
Matches 163; Conserva
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                                                                                                                                                                                                                                                                                                                                                        12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 WCRAGFEGKNCEL----DVTCNIKNGRCKQFCKLGPDNKVVCSCTTGYQLAEDQRSCEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SLYSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGYVSGWGRVFNKGRSASILQYLKVPLVDRATCLRSTKF----TIYNNMFCAGFHEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKRNVIRTILHHSYNATINKYNHDIALLELDEPLTLNSYVTPICIADREYSN...IFLKF
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                                                                                                                                                                                                                                                                                                                                                                                                                   GQFPWQVLLNGKVDAFCGGSIINEKWVVTAAHCIEPDVK----ITIVAGEHNTEKREHTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                     162-168,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 821; DB 1; 39.5%; Pred. No. 8.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                               from
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                                                                                                                                                                                                                                                               02-Aug-1996 #text_change
                                                                                                                                                      e sequences and
PMID:8168596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133;
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                                                                                                                                                                                                                      Harada,
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ng; carboxyglu
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                          homol
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447

387 329

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...vafu]i, T.; Maekawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A; Description: The cDNA cloninig and mRNA expression of rat A; Reference number: S18994
A; Accession: S18994
A; Status: preliminary
A; Molecule type: mRNA
A; Residues.
                                                                                                                                                                                                                                                                                                                                         B
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R:Okafuji, T.; Maekawa, K.; Mawa, K.; Marumoto, Y.
Blochim. Blophys. Acta 1131, 329-332, 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312; MUID:92329550; PMID:1627650
A;Reference number: S24312
A;Recession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 < COKA2>
A;Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F;137-057Domain: Gla domain homology < GT.A>
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Best Local S
Matches 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCAS-----
         HDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAF
                                                                                                                                  KVCPKGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANSFLEEVRAGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKYFDGDCCSTPPLDHQCD
                                                                                                TITKQGDSPWQAILLDSKKKLACGGVLIHTSWVLTAAHCLESSK---KLTVRLGEYDLRR
                                                                                                                                                                                                                      RCAPGYELADDHMHCRPTVNFPCGK----LWKRTDKKRKNFKRDIDPEDEELELGPRIVNG
                                                                                                                                                                                                                                                                              RCHEGYSLLADGVSCTPTVEYPCGKIPILEKRNASKPQG-------RIVGG
                                                                                                                                                                                                                                                                                                                                            SPCCGHGTCIDGLGGFSCSCDKGWEGRFCQQEMGFQ-DCRVKNGGCYHYCLEETRGRR-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSRDSCKGDSGGPHATRYRGTWYLTGIVSWGQGCAAVGH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGH 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.48;
37.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 775; DB 1;
Pred. No. 2.4e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 48;
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F;42-196,199-461/Product: protein C #status predicted <PRC>
F;42-196/Domain: light chain #status predicted <PCL>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
F;91-30/Domain: EGF homology <EG2>
F;91-461/Domain: heavy chain #status predicted <PCH>
F;39-411/Domain: activation peptide #status predicted <ACT>
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F;212-465/Domain: trypsin homology <TRY>
F;212-445/Domain: trypsin homology <TRY>
F;47,48,55,57,60,61,65,67,70,76,Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,388-426/Disulfide bonds: #s
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C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu
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F;253,299,402/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-33/Domain: signal F;27-85/Domain: Gla do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JX0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, J. Biochem. 111, 491-495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein C (activated) (EC 3.4.21.69) precursor - mouse N.Alternate names: vitamin K-dependent serine proteina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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         220
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159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein C is the zymogen of the vitamin K-dependent serine proteinase that
                                                                                                KGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCAS-----
                                                                                                                                                                              ACAPGYELADDHMRCKSTVNFPCGKLGRWIEKKRKILKRDTDLEDELEPDPRIVNGTLTK 219
                                                                                                                                                                                                                                                                                                 SPCCGHGTCIDGIGSFSCSCDKGWEGKFCQQELRFQDCRVN-NGGCLHYCLEESNGRR-C
                                                                                                                                                                                                                                                                                                                                                      SPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFLEEMRPGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKYFDGDQCSAPPLDHQCD
EQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-RF
                                                           QGDSPWQAILLDSKKKLACGGVLIHTSWVLTAAHC---VEGTKKLTVRLGEYDLRRRDHW 276
                                                                                                                                                                                                                                         RCHEGYSLLADGVSCTPTVEYPCGKIP--ILEKRNASK------PQGRIVGGKVCP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMRSEPRPGVLLRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIIGDTRDACDGDSGGPMVVFFRGTWFLVGLVSWGEGCGHLNNYGVYTKVGSYLKWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQK 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQETVVTGWGYQSDKVKDGRRNRTFI-LTFIRIPLAARNDCMQVMNNV-----VSENMLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDPWELDLDIKEVLVHPNYTRSNSDNDIALLRLSQPATLSKTIVPICLPNSGLAQELSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 769; DB 1;
Pred. No. 6.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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278

52

101

159

# # S

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G:Comment: Protein C is synthesized in the liver as a single chain precursor, which is contined to the stratecapeptide from the amino end of the heavy chain; this reacting comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stratecition of the thrombin-thrombomodulin complex.

G:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitaming C:Superfamily: coagulation factor x; EGF homology; Gla domain homology; trypsin homology; (Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding p:1-29/Domain: signal sequence (fragment) #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 197-454, 'PV' <STE>
A; Residues: 197-454, 'PV' <STE>
R; Esmon, N.L.; DeBault, L.E.; Esmon, C.T.

J. Blol. Chem. 258, 5548-5553, 1983
A; Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless A; Reference number: A37541; MUID: 83213513; PMID: 6304092
A; Contents: annotation; activation; calclum binding
R; Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Blol. Chem. 258, 5554-5560, 1983
A; Title: Structural changes required for activation of protein C are induced by Ca2+ bi A; Reference number: A37542; MUID: 83213514; PMID: 6406503
A; Contents: annotation; activation; calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.A;Reference number: A26250; MUID:85014826; PMID:6091100
A;Accession: A26250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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N; Residues: 40-194 <FER>
N; Residues: 40-194 <FER>
N; Residues: 41-198 was also found
N; Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
N; Title: beta-Hydroxyaspartic acid in vitamin K-dependent |
N; Reference number: A19316; MUID:83169769; PMID:6572939
N; Contents: annotation; revision to residue 110
N; Stenflo, J.; Fernlund, P.;
N; Stenflo, J.;

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3.71tle: Amino acid sequence of the light chain of bovine protein

3.7Reference number: A18385; MUID:83007325; PMID:6896876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Molecule type: mRNA
N; Residues: 1-456 <LON>
R; Fernlund, P.; Stenflo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i; Alternate names: autoprothrombin IIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Biol. Chem. 257, 12180-12190, 1982
;Title: Amino acid sequence of the heavy chain of bovine;Reference number: A18386; MUID:83007326; PMID:6896877;Accession: A18386
                                                                            24-83/Domain: Gla domain homology <GLA>
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Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
Accession: A26250; A18385; A18386; A00928
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propeptide #status predicted <PRO>
t: protein C light chain #status experimental <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on; activation; calcium binding is the zymogen of the vitamin K-dependent serine proteinase that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;197-210/Domain: activation peptide #status experimental <APT>
F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:197-456/Product: protein C heavy chain #status experimental <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;98-128/Domain: EGF homology <EG1>;137-172/Domain: EGF homology <EG2>
  447
                                        394
                                                                                387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 LPCCGRGKCIDGLGGFRCDCAEGWEGRFC-LHEVRFSNCSAENGGCAHYCMEEEG-RRHC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 SPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQC-----AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.2%; Score 749; DB 1; Similarity 38.7%; Pred. No. 2.1e-48;
QEAP
                                                                                                           DGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRS 393
                                                                                                                                                                                                                                                                                                                 PKGECPWQVLLLVNGAQL-CGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDG 218
                                                                                                                                                                                                                                                                                                                                                                                                SCAPGYRLEDDHQLCVSKVTFPCGRLGKRMEKKRKTLKRDTNQVDQKDQLDPRIVDGQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                     RCHEGYSLLADGVSCTPTVEYPCGKI-PILEKRNAS------KPQ--GRIVGGKVC 159
                                        EPRP
                                                                     GDPRDACEGDSGGPMVTFFRGTWELVGLVSWGEGCGRLYNYGVYTKVSRYLDWIYGHIKA 446
                                                                                                                                                                                           FSLVSGWGQLLDRGAT----ALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYS 333
                                                                                                                                                                                                                                     WEVDLDIKEVIIHPNYTKSTSDNDIALLRLAKPATLSQTIVPICLPDSGLSERKLTQVGQ
                                                                                                                                                                                                                                                               DEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFV-R 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLEELRPGNVERECSEEVCEFEEAREIFQNTEDTMAFWSFYSDGDQCEDRPSGSPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
450
                                                                                                                                                     RDETKRNRTFVLSFIKVPVVPYNACVHAMEN----KISENMLCAGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid (Glu)
                                                                                                                                                                                                                                        334
                                                                                                                                                     386
                                                                                                                                                                                                                                                                                                                      274
                                                                                                                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bonds:
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Search completed: July 1, 2003, 17:54:33 Job time: 43 secs